

METATRANSCRIPTOME ANALYSES AND RESEARCH TOPICS

Single genome

- Map reads to genome
- Cell metabolism & regulation



de novo assembly

- Few or no sequenced genomes
- Target genes & pathways
- Species interactions & signaling



Read-based surveys

- Few or no sequenced genomes
- Target genes & pathways where databases exist
- Metabolic networks

		Read based					Assembly based		
		MetaTrans	COMAN	FMAP	SAMSA2	HUMAnN2	SqueezeMeta	IMP	MOSCA
Preprocessing	QC	✓	✓	✓	✓	×	✓	✓	✓
	Removes host reads	×	×	✓	×	×	×	✓	×
	Removes rRNA	✓	✓	×	✓	×	✓	✓	✓
<i>de novo</i> Assembly		×	×	×	×	×	✓	✓	✓
Binning		×	×	×	×	×	✓	✓	×
Taxonomic	Reads	✓	✓	×	✓	✓	×	×	×
Profiling	Contigs	×	×	×	×	×	✓	✓	✓
Functional	Reads	✓	✓	✓	✓	✓	×	×	×
Annotation	Contigs	×	×	×	×	×	✓	✓	✓
Pathway Analysis		✓	✓	✓	×	✓	✓	✓	×
Requires Metagenomes		×	×	×	×	×	×	✓	×
Summary Report		×	×	×	×	×	×	✓	×
Web Interface		×	✓	×	×	×	×	×	×
Multiple Sample Comparisons		✓	✓	✓	✓	✓	✓	×	✓
Differential Expression		✓	✓	✓	✓	×	×	×	✓
Docker		×	×	×	×	✓	×	✓	✓
Conda		×	×	×	×	✓	×	✓	×
Long Read Support		×	×	×	×	×	✓	×	×
Public Code Repository		✓	×	✓	✓	✓	✓	✓	✓

Schematic summary of the analysis

